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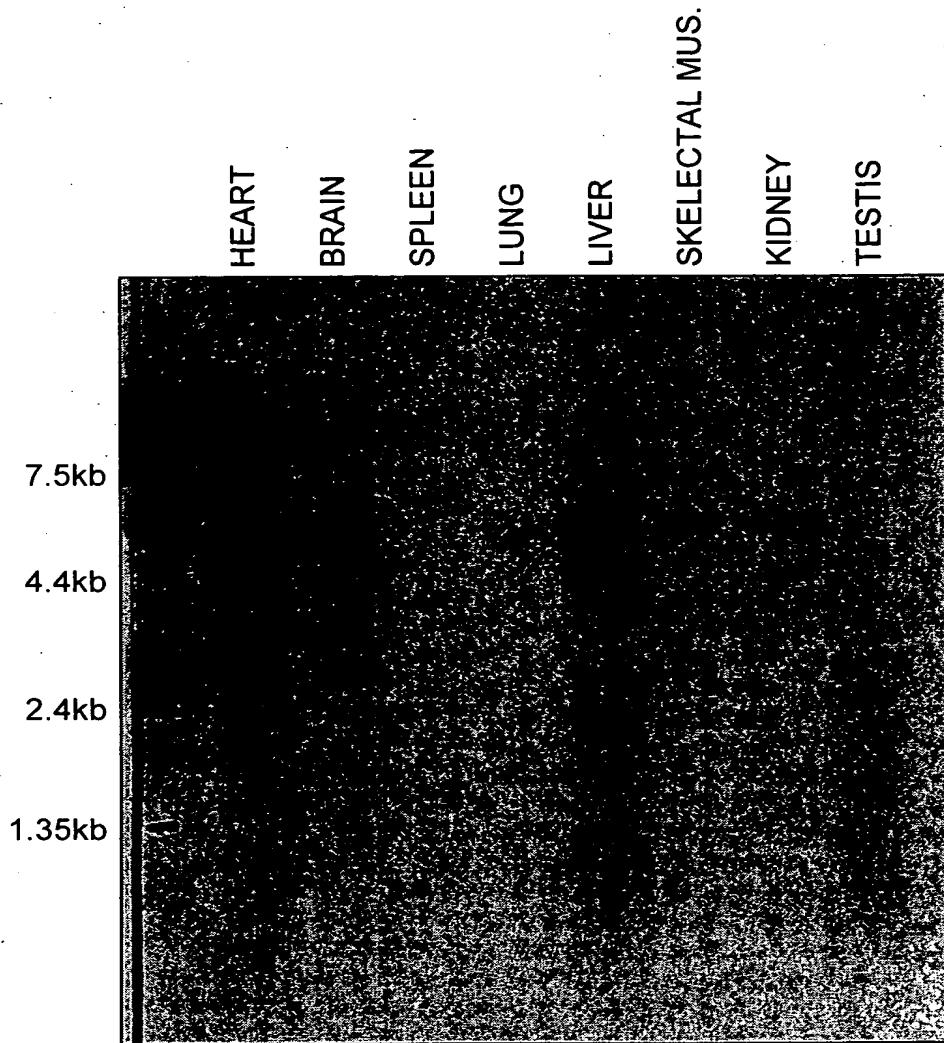


FIG. 1
MURINE MTN BLOT PROBED WITH
 ^{32}P -LABELLED MURINE PDE_XIV



MOUSE EMBRYO

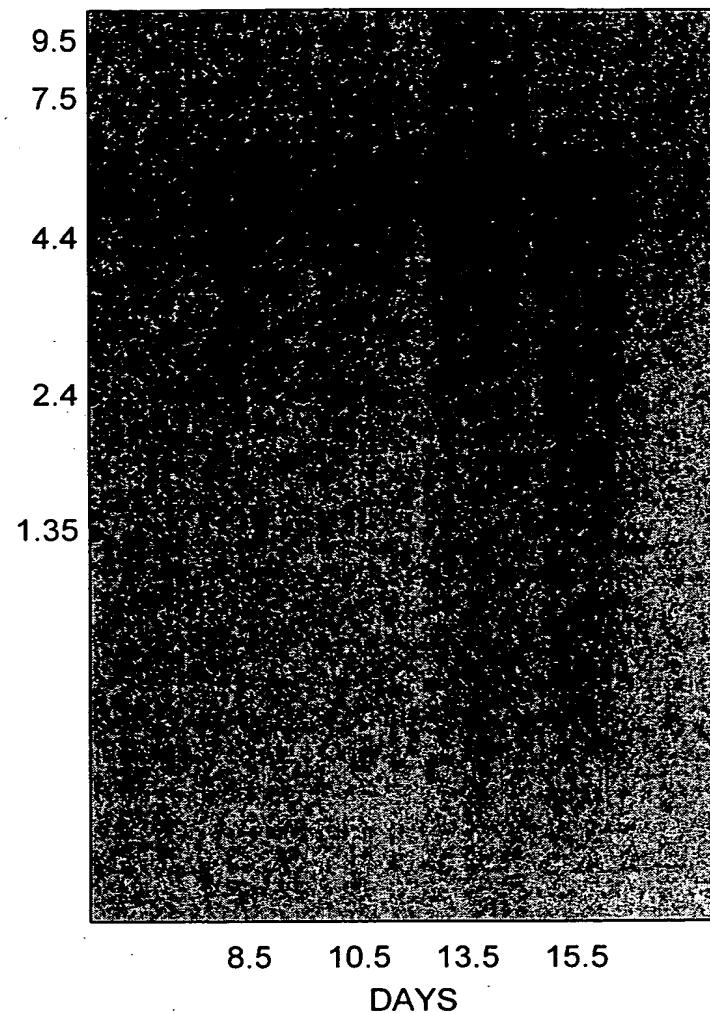


FIG. 2

MURINE EMBRYO MTN BLOT PROBED
WITH ^{32}P -LABELLED MURINE PDE_XIV



A	1	2	3	4	5	6	7	8
WHOLE BRAIN	AMYG- DALA	CAUDATE NUCLEUS	CERE- BELLUM	CEREBRAL CORTEX	FRONTAL LOBE	HIPPO- CAMPUS	MEDULLA OBLON- GATA	
OCCIP- ITAL LOBE	PUTAMEN	SUBST- ANTIAL NIGRA	TEMP- ORAL LOBE	THALA- MUS	NUCLEUS ACCUM- BEUS	SPINAL CORD		
HEART	SORTA	SKELETAL MUSCLE	COLON	BLADDER	UTERUS	PROST- ATE	STOMACH	
TESTIS	OVARY	PANC- REAS	PITUIT- ARY GLAND	ADRENAL GLAND	THYROID GLAND	SALIVARY GLAND	MAMM- ARY GLAND	
KIDNEY	LIVER	SMALL INTE- STINE	SPLEEN	THYMUS	PERIPH- ERAL LEUKO- CYTE	LYMPH NODE	BONE MARROW	
APPEN- DIX	LUNG	TRACHEA	PLACEN -TA					
FETAL BRAIN	FETAL HEART	FETAL KIDNEY	FETAL LIVER	FETAL SPLEEN	FETAL THYMUS	FETAL LUNG		
YEAST TOTAL RNA 100ng	YEAST tRNA 100ng	E. COLI rRNA 100ng	E. COLI DNA 100ng	POLY r(A) 100ng	HUMAN C ₁₁ DNA 100ng	HUMAN DNA 100ng	HUMAN DNA 500ng	

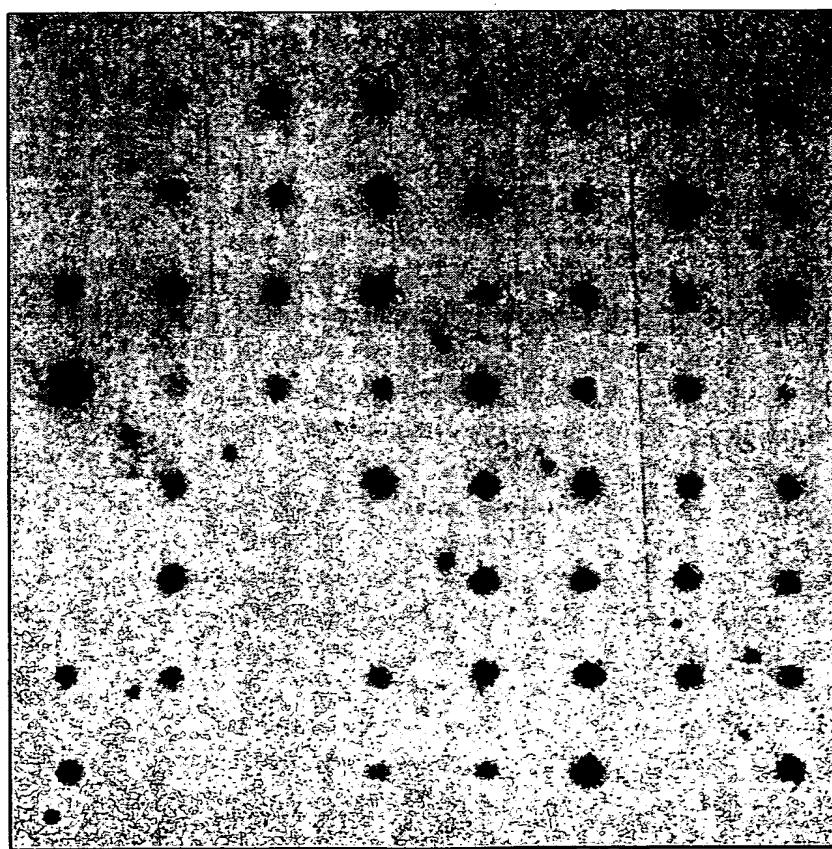


FIG. 3
HUMAN RNA MASTER BLOTH PROBED WITH
 ^{32}P -LABELLED HUMAN PDE_XIV



FIG. 4

Alignment of the Murine and Human PDE_XIV nucleotide sequence

New sequence is PDE_XIV

Pileup: Genetics Computer Group.
MSF: 3134 Type: N Check: 5422 ..

Name: mpdea_ oo Len: 3134 Check: 5084 Weight: 0.001
Name: hspdea_ oo Len: 3134 Check: 338 Weight: 0.100

new mpdea_	1 AGGTACGCCT GCAGGTACCG GTCCGGAATT CCCGGGTCGA CCCACGCGTC
new hspdea_
new mpdea_	51 CGGCCAGCCT CCCAGGCCGG CTGCCTGCTC ACCCAGCCAG TCGCTAGCTC
new hspdea_	1
mpdea_	101 TGGGCACTGC AGCAGGCTCG GCTCTGTCCC AGCGCTCGCT TGCTTGCTCG
hspdea_	9 GATGCAGTGC AGCAGGCTCG GCTCTGTCCC AGC....A..
mpdea_	151 CTCGCTCGGC TGGGAGAAAA GTGGTGTC.C TCGCCCAG.. AGAGCCTCTC
hspdea_	43CTTGTC TGGGAGAAAA GTGGTGTTAC TCACCCAGGG AGAGTCTCTC
mpdea_	198 TCTC..CCTT CCTTCTTTCT CGAGCTCTCT GAGTCCTTTG GCGTTTCTTT
hspdea_	89 TTTCTACCTT CCTTCTTTCT CGATCTCCTT GTGTGCTTTT GTGTGCTTT
mpdea_	246 CTTTCTTTCC TTTTTTTTTT TTTTTTAATA TTTTCTTTTT CTTTCTATAAA
hspdea_	139 ATTTCTTTTC CTTTTTTTTT TT..... TTTTTTTTTT GTTACT....
mpdea_	296 AACTTGCATA ATTATACTGC TAATCCTGGA TGAGGTTGCT GGATTCTGCA
hspdea_	177TA ATTATATTCC TAATCCTGGA TGAAGGTTGCT GGATTCTGCA
mpdea_	346 GCACAAATCT TCATGAACAA GCCGCACCGC TCAGAGATTT CACAGCATTC
hspdea_	219 GCACAAAGTCT TCATGAACAA GCAGCACCGC TCAGAGATTT CACGGCATTC
mpdea_	start codon
hspdea_	396 AAAGGTCACA GAACTGCCAC TATGGTTAAA <u>TGTCTTGTTT</u> AATGGTTGAG
mpdea_	269 AAAGGTCACA GAACTGCCAC TATGGTTAAA <u>TGTCTTGTTT</u> AATGGTTGAG
hspdea_	446 AGGTGTGGCG AAGTCTTGTGTT TGAGAGCCCT GAACAGAGTG TCAAATGTGT
mpdea_	319 AGGTGTGGCG AAATCTTGTGTT TGAGAACCCC GATCAGAATG CCAAATGTGT
hspdea_	496 TTGCATGCTA GGAGATGTAC GACTAAGGGG TCAGACGGGG GTTCCTGCCG
mpdea_	369 TTGCATGCTG GGAGATATAC GACTAAGGGG TCAGACGGGG GTTCGTGCTG
hspdea_	546 AACGCCGTGG CTCCTACCCA TTCATTGACT TCCGTCTACT TAACAATACA
mpdea_	419 AACGCCGTGG CTCCTACCCA TTCATTGACT TCCGTCTACT TAACAGTACA
hspdea_	596 ACACACTCAG GGGAAATTGG CACCAAGAAA AAGGTGAAAC GACTGTTAAG
mpdea_	469 ACATACTCAG GGGAGATTGG CACCAAGAAA AAGGTGAAA GACTATTAAG
hspdea_	646 TTTCAAAGA TACTTCCATG CATCTAGGCT TCTCCGGGGG ATTATACCGC
mpdea_	519 TTTCAAAGA TACTTCCATG CATCAAGGCT GCTTCGTGGA ATTATACAC
hspdea_	696 AGGCCCTCT CCACCTGCTG GATGAAGACT ACCTTGGACA AGCAAGGCAC
mpdea_	569 AAGGCCCTCT GCACCTGCTG GATGAAGACT ACCTTGGACA AGCAAGGCAT
hspdea_	746 ATGCTCTCCA AAGTTGGAAC GTGGGACTTT GACATTTCT TGTTGATCG
mpdea_	619 ATGCTCTCCA AAGTGGGAAT GTGGGATTTT GACATTTCT TGTTGATCG



FIG. 4 CONT'D

mpde_ 796 CTTGACAAAT GGGAACAGTC TGGTAACCTCT GTTGTGTCAC CTCTTCAACT
 hspde_ 669 CTTGACAAAT GGAAACAGCC TGGTAACACT GTTGTGCCAC CTCTTCAAATA

 mpde_ 846 CCCATGGGCT CATCCACCAT TTCAAGCTCG ATATGGTGAC CTTGCACAGG
 hspde_ 719 CCCATGGACT CATTACACCAT TTCAAGTTAG ATATGGTGAC CTTACACCGA

 mpde_ 896 TTTCTGGTTA TGGTTCAAGGA AGATTACAC GGTACAAACC CATAACACAA
 hspde_ 769 TTTTTAGTCAGA TGGTTCAAGGA AGATTACAC AGCCAAAACC CGTATCACAA

 mpde_ 946 TGCTGTTCAC GCAGCCGACG TCACCCAGGC CATGCACTGT TACCTGAAGG
 hspde_ 819 TGCTGTTCAC GCAGCCGACG TCACCCAGGC CATGCACTGC TACCTGAAAG

 mpde_ 996 AGCCAAAGTT GGCAAGCTTC CTCACACCTC TGACATCAT GCTTGGACTA
 hspde_ 869 AGCCAAAGCT TGCCAGCTTC CTCACGCCCTC TGACATCAT GCTTGGACTG

 mpde_ 1046 CTGGCTGCAG CAGCTCATGA CGTGGACAC CCAGGGTCA ACCAGCCATT
 hspde_ 919 CTGGCTGCAG CAGCACACGA TGTGGACAC CCAGGGTGA ACCAGCCATT

 mpde_ 1096 TTTGATCAAA ACTAACCAAC ATCTTGCCAA CCTGTATCAG AATATGTCTG
 hspde_ 969 TTTGATAAAA ACTAACCAAC ATCTTGCAAA CCTATATCAG AATATGTCTG

 mpde_ 1146 TACTGGAGAA TCACCACTGG CGATCTACAA TTGGCATGCT TCGAGAACATCA
 hspde_ 1019 TGCTGGAGAA TCATCACTGG CGATCTACAA TTGGCATGCT TCGAGAACATCA

 mpde_ 1196 CGGCTCCCTGG CTCACTTGCC AAAGGAAATG ACACAGG... ATATC
 hspde_ 1069 AGGCTCTTG CTCATTTGCC AAAGGAAATG ACGTAAGTGC TGCCGAGATG
 stop codon

 mpde_ 1238 GAACA..... GCA..... GCTG GGCTCCCTCA TCTTGGCCAC
 hspde_ 1119 AAACATACTG ATGTGCATGC AGTAAAGATA AGCCACTTTC TCTAGGGCA

 mpde_ 1270 GGATATCAAC AGACAGAACATG AGTTTCTGA. CCCG CTTAAAAGCT
 hspde_ 1168 GGCTTGGGAC CTTTGCGTG AATGGCAGAG AGCCCCCCCAGG CTGTACTTCC

 mpde_ 1313 CACCTCCACA ATAAAGATT. TGAGAC. TGGAGAAC GT.ACAGGA.
 hspde_ 1218 TGCCTGCACT GAGCTGTCTA TCAGAGGAGA TTTGGTGTCA GTTACAGCAA

 mpde_ 1354 ..CAGACACT TTATGCT.TC AGATGCCCTT GAAGTGTGCT GACATTGCA
 hspde_ 1268 CCCAGAAACC AAAATCTCTC TGTGTGCTTT GAAAGGGCCT TGCAGAGTCA

 mpde_ 1401 AT..CCTT.. GTC.GTATCT GGGAGATGAG CAAGCAGT.. GGAGTGAAAG
 hspde_ 1318 ATGACCTACA GTCAGGAAAA GGGATAATAA ACAGCTCTCA GTTTTCACAC

 mpde_ 1444 GGT..... CTGTGAGGAA TTCTACAGAC AAGGTGACCT TGAAC.. AG.
 hspde_ 1368 GCTTCAGTAT CAGTGCTCAA CTTTGCCAAA TTCCCGACCT TTAGTTAGC

 mpde_ 1484 AAGTTGAAC TGGAATCAG .TCCTCTTG TAATCAAC.A GAAAGATTCA
 hspde_ 1418 AAAATTGTCC TTCCATGTAG CTCCAAATAG TAAATATTCA TCAAGAAGGA

 mpde_ 1532 ATCCCTAGCA TACAAA... T TGGTTTCATG ACT.TACATC GTGGAGCCGC
 hspde_ 1468 A.CCCAGGCA TTCTAAAGCT AGAGTCAAA AAAGTATATT TTGTAATTGC

 mpde_ 1578 TGTTCCGGG.AGTGG.. GCCCCGGTTA CTGGG.. AAC AGCACCCCTGT
 hspde_ 1517 TAGTCTCAGC AAAAATAGAA GTCAGAAATT CTTTCTAAA ATGTCTTTG

 mpde_ 1620 CGGAGAACAT GCTAAGCC.ATCTCG CGCACAACAA AGCCCAGTGG
 hspde_ 1567 CTAAGTAATT GAAATGGCCC TAGCATTTC TTCACCAATT AATTACCTT

 mpde_ 1664 AAGAGCCT.G CTGTCCAATC AGCAC... AG ACGCA.GGGGCAG
 hspde_ 1617 ACGTCTCTTG CACTTAAAC AGAAGGGAG ACACTCATTT TCTGGTTCAAC

 mpde_ 1702 CG.....G CCAGGACCTG GCGG....GC CCCGC... AC CTGAGACCCT
 hspde_ 1667 TATTTGATAG CCATGGTATG TAGGCTGAGT CCCACTAAAT CTGAGGCCAT



FIG. 4 CONT'D

stop codon

mpde_ 1738 GGAG.CAGAC AGAAGGTGCC ACGCCTAAG GTAGCTGTC. .TGCTGA.. T
hspde_ 1717 TGTTTCATTT TCCTGGTG. . .GCCCAAG TTAGCTGCTA ATACTGTCTT

mpde_ 1783 GCACGGCCA. TCT G. TCCGTCCA CAGGA GCACGGCC..
hspde_ 1763 CCAAGGCCAC CATTAAATTCT GATCTGTTA ATGAACACGT GCAGAACCAA

mpde_ 1817 ...ATCC... G TCC... GACT GC.CCTCGCAAC
hspde_ 1813 AGAAACCTAG GTGAAAAGAG TACATAGATT GCTGTACCC TCTTCAAGAC

mpde_ 1840 AAGCCCATCA CGCTGGGTT CGATGCCAT. .CCGCCTGCC A.CTTACC..
hspde_ 1863 AAGCACATAA CTTGAGGTCA AGGACCAAGT GCTGTCTCCC AACTGAACAA

mpde_ 1885 ...GCCTCCC TTCGTTGATC CAAGTGTACA AAAGCCATTG ...TCACCTC
hspde_ 1913 GCAGTATACT CTGGGTTGTG GATTGATTCC TGGCCCTCTG ATTTGATCTC

mpde_ 1929 AGCAT.TAGCTGCC. ..GAAATGGG CGGCTCTATC CCGTCATTGG
hspde_ 1963 ATGCTGTTTC CTAGCACCCA GAGGAATGTG AAATTGAG GAGGAATTTC

mpde_ 1970 AG..CTGAT. TCTGGGG CGGCTGCCAACCGAAAC.G
hspde_ 2013 AGTTCTGATA AATTTTACT CCCTGGAACT AAATAAAACC AGTTCTCGTG

mpde_ 2004 CCTGGAAGTA AGAA..AGGG GTGCTTCTGC CGTGTTGCC TCTGGCCCTT
hspde_ 2063 CATGGAATAA AAACTTATGC CTCTTACTAG AATAATAAT TGCAAAGATT

mpde_ 2052 GGTCACGCTG ACTGGCAGTA GCTCCTAAGT CCAGAGCATT TTAACGTTTG
hspde_ 2113 GAAAGAATTA AATGCAAAAA GAACTAAAAA CTAGAGCAAA AGATCAAGTG

mpde_ 2102 CCATC..GGA CAGCTGACCT ...GCATGAC ACCAGCAT.. .ACTTGGAAC
hspde_ 2163 AGAAGAAGAA AAGAGGAGGT AAGGAGAGAG ACAAGGAAGA AAGAAGGAGA

mpde_ 2144 TGCAAAACTG GTCTTGCCTG CCAGAGCACA AACGAGAGTG TGAGAGAAA.
hspde_ 2213 AGGAAAGGAA GAATAGTGAG G.ACAGGAAA GAAGAAAATG CAAGGGAAAT

mpde_ 2193 ..GTACCTTC TATTT..TAA TAATAATTAT TATTATAAAA TA....ATAA
hspde_ 2262 GGGAAAGGAC TCTGGGGTGA CCAGACTTCT CCTGGTCAGT ACCTGCATTG

mpde_ 2235 ATCTTTTAA CTTT..ATA TTTCATGCAC CAGACAATGG GTCTAAAATC
hspde_ 2312 ATCCTGTTG TTACTCAATA TTTCTTCCT AAAATATTCA TTTCACATCT

mpde_ 2283 TTGGA...CA AGTAATACTC TGCGTACCCA AACCTAAGAG G....GGG
hspde_ 2362 ATGGATTCCA ATGAAAAATA TATTTTATG TGTCTTTGTG GAACACAGTG

mpde_ 2324 TTC...ATTA TTTT.GCTAT T.GACTC... .TATGCCAC ATTGGGTCCG
hspde_ 2412 TTATAAAATTG TTTTGCCAG AAGAATAATT GTTATACAAT AATATATGTG

mpde_ 2364 AGA..TGTGG CACCATTGCG ATTTCTGAAA CCACGCGTCC .CCTCCCAC
hspde_ 2462 AAAACTTTAT TACAAAAGCC ATTATCATAA TCATTATTAT TCCTTCTATC

mpde_ 2411 TGGTCCAAGG TGCTGTACAG CCCGTCCC... .TTTGACCC GTTAGCCAAAT
hspde_ 2512 ACA.GGTAAA TGCTTTAATG TCATTTTCT GATTTAAAAA GTAGGGCAGG

mpde_ 2457 CCGTCTT... .TACGGA ...TTCAGTG ACCTGTTAT ATTACCAA.G
hspde_ 2561 TTAATTGTAG AAAGTAAGGA AAATTCAAGGA AAGTGTAGT TTGAACATATG

mpde_ 2497 TGTACATTTC CTGT..AAAT ACCAAACGCT ACTGA.... .TTCC
hspde_ 2611 TGAAGTTGCT CTTTTAAGG GCCAAAAACA GGAGACTTT AGCACTTTCA

mpde_ 2534 CATGC..CA.AAATAC ACGAGTATTA TGGGATTGCT A....CCTG
hspde_ 2661 TATGTTTCAG CTTGATATGA AAGAGAAAAC TGAAACTGCT AGTAATCCTG

mpde_ 2571T ATAAAACAATG GCACTGTGAA CAGAATA... .CTGTTAGTT
hspde_ 2711 CCATCCAGGT ATAGTTCATG TTAACCTGGC TAGTTTATTT TCTTTAGTC



FIG. 4 CONT'D

mpde_	2608 TTAATACAAG AGAATGCATT TGTAATATG GTATAGAGTT TATTAATATA
hspde_	2761 TTTTTCAAT ACAAA. CTTA TTTAACAAA ATAT. GATTA TATTGGGA
mpde_	2658 CTGTTGTTCG CAGATAAAGG CCTTAACCTT AAAAAAAAAA AAAAAAAAA.
hspde_	2809 ACTTATTTA CAGTTACGT CCTGAAATT TTATTTACA ATAAAGACTT
mpde_	2708 AAAA AAAAAAAAAA AAAAGGGGC GGCGCTCTA GAGGATCCCT
hspde_	2859 TTTTCAAAT CAAAAAAA AAAAAGGGC GGCGCTCTA GAGGATCCCT
mpde_	2752 CGAGGGGCC AAGCTTACGC GTGCATGCGA CGTCATAGCT CTCTCCCTAT
hspde_	2909 CGAGGGGCC AAGCTTACGC GTGCATGCGA CGTCATAGCT CTCTCCCTAT
mpde_	2802 AGTGAGTCGT ATTATAAGCT AG. 2823
hspde_	2959 AGTGAGTCGT ATTATAAGCT AGGCACTGGC CGTC 2992



FIG. 5

Protein Alignment of the Murine & Human PDE XIV

CLUSTAL W (1.7) multiple sequence alignment

mpde hspde	MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLNNNTTHS MSCLMVERCGEILFENPDQNAKCVCMGLDIDLRLRGQTGVRAERRGSYPFIDFRLNNSTTYS	60 60
mpde hspde	GEIGTKKKVKRLLSFQRYFHASRLLRGIIPOAFLHLLDEDYLGQARHMLSKVGTWDFDIF GEIGTKKKVKRLLSFQRYFHASRLLRGIIPOAFLHLLDEDYLGQARHMLSKVGMWDFDIF	120 120
mpde hspde	LFDRLTNGNSLVTLCLHFNSHGLIHHFKLDMVTLHRFLVLMVQEDYHGHNPYHNAVHAAD LFDRLTNGNSLVTLCLHFNTHGLIHHFKLDMVTLHRFLVLMVQEDYHSQNPHYHNAVHAAD	180 180
mpde hspde	VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAHDVDHPGVNQPFLIKTNHHHLANLYQNMS VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAHDVDHPGVNQPFLIKTNHHHLANLYQNMS	240 240
mpde hspde	VLENHHWRSTIGMLRESRLLAHLPEKMTQDIEQQLGSLILATDINRQEFLTRLKAHLHN VLENHHWRSTIGMLRESRLLAHLPEKMT-----	300 268
mpde hspde	KDLRLENVQDRHFMLQIALKCADICNPCTIWEWSKQWSERVCEEFYRQGDLEQKFELEIS	360
mpde hspde	PLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSSLNSQ	420
mpde hspde	HRRRGSGQDLAGPAPETLEQTEGATP	446

Zinc binding motif's are highlighted in **bold**.
Non-Catalytic domain in *italics*.

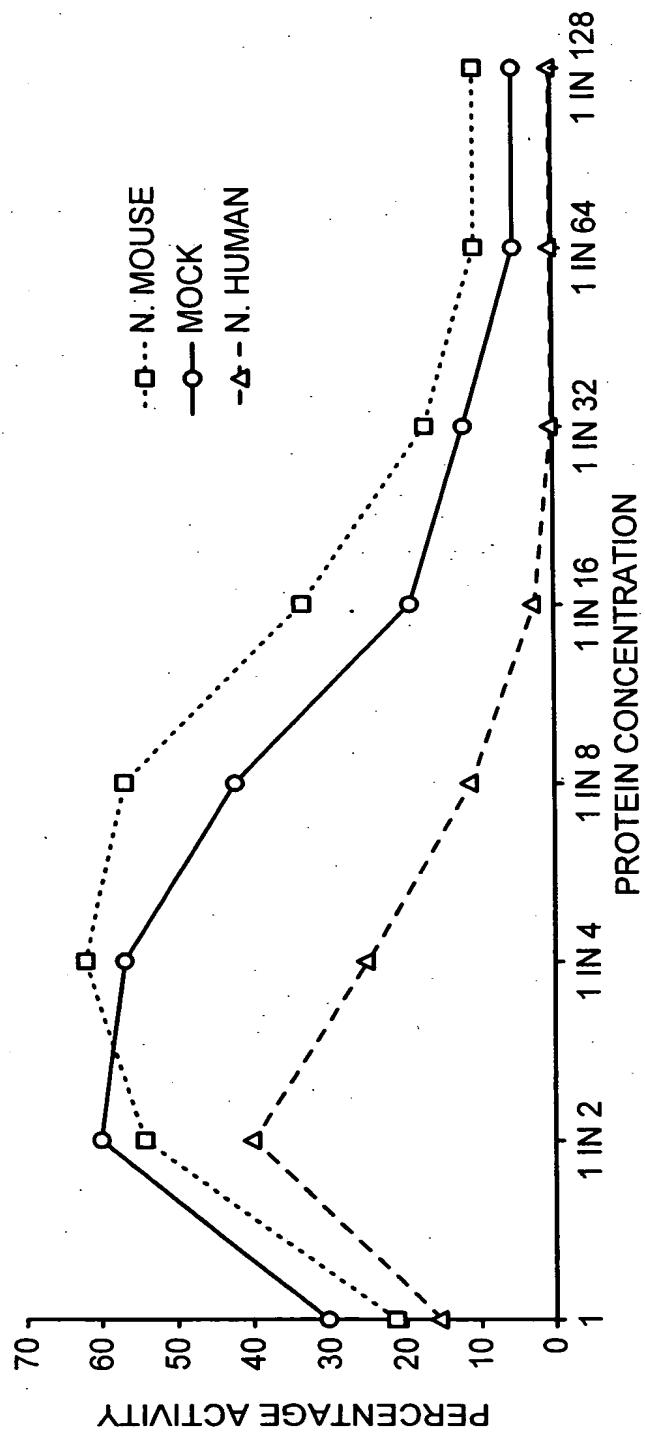


FIG. 6

SPA ASSAY TO DETERMINE THE CAMP HYDROLYTIC
ACTIVITY OF MURINE AND HUMAN PDE_XIV